

Amendt A

#6



SEQUENCE LISTING

<110> Fish B. A. D. M. B.
Kang, Dong-Chul
Gopalkrishnan, Rahul V.

<120> USE OF MDA-5 AS AN ANTIVIRAL AND
ANTIPROLIFERATIVE AGENT

<130> A34614-A-PCT-USA-A (070050.1921)

<140> 10/055,475
<141> 2002-01-22

<150> PCT/US01/06960
<151> 2001-02-28

<150> 09/515,363
<151> 2000-02-29

<160> 17

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 3365
<212> DNA
<213> homo sapiens

<400> 1
gcgcgcggc ctgagagccc tgtggacaac ctgcgtcattt tcagggcacag agcggttagac 60
cctgcttc taagtggca gcggacagcg gcacgcacat ttccacctgtc ccgcagacaa 120
cagcaccatc tgcttggag aaccctctcc ttctcttag aagaaaagat gtcgaatggg 180
tattccacag acgagaattt ccgttatctc atctctgtct tcagggccag ggtgaaaatg 240
tacatccagg tggaggctgt gctggactac ctgaccccttc tgccctgcaga ggtgaaggag 300
cagattcaga ggacagtcgc caccccgagg aacatgcagg cagttgaact gctgctgagc 360
accttggaga agggagtctg gcaccttggt tggactcggg aatttcgtgga gcccctccgg 420
agaacccgca gcccctctggc cgcccgctac atgaacccctg agctcacggc cttgcctct 480
ccatcggtttt agaacgcgtca tgatgaatat ctccaaactgc tgaaccccttc tcagcccaact 540
ctgggtggaca agcttctagt tagagacgtc ttggataagt gcatggagga ggaactgttg 600
acaatttgaag acagaaaaccg gattgctgtc gcagaaaaaca atggaaatga atcaggtgt 660
agagagctac taaaaaggat tttgtcagaaa gaaaactgtt tctctgtcatt tctgaatgtt 720
cttcgtcaaa caggaaacaa tgaacttgc caagagttaa caggctctga ttgctcagaa 780
agcaatgcag agatttggaaa tttatcacaa gttgtatggc ctcaagtggaa agagcaactt 840
ctttcaacca cagttcagcc aaatctggag aaggaggtct ggggcattggaa gaataactca 900
tcagaatcat cttttgcaga ttcttctgtt gtttcagaat cagacacaag tttggcagaa 960
gaaagtgtca gctgtttaga tgaaagtctt ggacataaca gcaacatggg cagtgattca 1020
ggcacccatgg gaagtgttcc agatgttggaa aatgtggcag caagagcatc cccggagcca 1080
gaactccagc tcaggcccttta ccaaattggaa gttgcccagc cagccttggaa agggaaagaaat 1140
atcatcatct gcctccctac agggaggtggaa aaaaccagag tggctgttta cattgccaag 1200
gatcacttag acaagaagaa aaaaggatctt gaggctggaa aagttatagt tcttgcataat 1260
aaggtaactgc tagttgaaca gctttccgc aaggagttcc aaccattttta gaagaaatgg 1320
tatcgtgttta ttggatttttggatacc caactgaaaa tatcattttcc agaagttgtc 1380
aagtccctgtg atattattt cagttacagct caaatcccttggaa aaaaactccctt cttaaacttgg 1440
gaaaatggag aagatgttgg tggatccattt tcagactttt ccctcattat cattgatggaa 1500
tgtcatcaca ccaacaaaga agcagtgtat aataacatca tgaggcatta tttgtatgcag 1560

aagggtaaaa	acaatagact	caagaaaagaa	aacaaaccag	tgattccct	tcctcagata	1620
ctgggactaa	cagcttcacc	tggtgttgg	ggggccacga	agcaagccaa	agctgaagaa	1680
cacattttaa	aactatgtgc	caatcttgc	gcatttacta	ttaaaactgt	taaagaaaac	1740
cttgcataac	tgaaaaacca	aatacaggag	ccatcgaaaga	agtttgccat	tgcagatgca	1800
accagagaag	atccattaa	agagaaaactt	ctagaaaataa	tgacaaggat	tcaacttat	1860
tgtcaaatga	gtccaaatgtc	agattttgg	actcaaccct	atgaacaatg	ggccattcaa	1920
atggaaaaaa	aagctgcaaa	aaaaggaaat	cgcaaaagaac	gtgtttgtc	agaacatttg	1980
aggaagtaca	atgaggccct	acaaaattaat	gacacaattc	aatgatgata	tgcgtatact	2040
catcttgc	ctttctataa	tgaagagaaaa	gataagaagt	ttgcagtcat	agaagatgat	2100
agtgtgtgagg	gtgggtgtga	tgagtattgt	gatgggtatg	aagatgagga	tgatttaaag	2160
aaaccttga	aactggatga	aacagataga	tttctcatga	ctttatTTT	tgaaaacaat	2220
aaaatgttga	aaaggctggc	tgaaaaccca	gaatatgaaa	atgaaaagct	gaccaaatta	2280
agaaaatacca	taatggagca	atatactagg	actgaggaat	cagcacgagg	aataatctt	2340
acaaaaaacac	gacagagtgc	atatgcgtt	tcccagtgg	ttactgaaa	tgaaaatattt	2400
gctgaagtag	gagtcaaagc	ccaccatctg	attggagctg	gacacagcag	tgagttcaaa	2460
cccatgacac	agaatgaaca	aaaagaagtc	attagtaat	ttcgcactgg	aaaatcaat	2520
ctgcttatcg	ctaccacagt	ggcagaagaa	ggctggata	ttaaagaatg	taacattgtt	2580
atccgttatg	gtctcgatc	caatgaaata	gccatggtcc	aggcccggtg	tcgagccaga	2640
gctgtatgaga	gcacctacgt	cctgggtgt	cacagtggtt	caggagttat	cgaacatgag	2700
acagttaatg	atttccgaga	gaagatgatg	tataaagcta	tacattgtgt	tcaaaatatg	2760
aaaccagagg	agtatgctca	taagattttg	gaattacaga	tgcaaaagtat	aatggaaaag	2820
aaaatgaaaa	ccaaagagaaa	tattgccaag	cattacaaga	ataacccatc	actaataact	2880
ttccttgca	aaaactgcag	tgtgctagcc	tgttctgggg	aagatatcca	tgtatttgag	2940
aaaatgcattc	acgtcaatat	gaccccagaa	ttcaaggaac	tttacattgt	aagagaaaac	3000
aaagcactgc	aaaagaagtg	tgccgactat	caaataatg	gtgaaatcat	ctgcaaatgt	3060
ggccaggcgtt	ggggaaacaat	gatggtgac	aaaggcttag	atttgccctt	tctcaaaaata	3120
aggaattttg	tagtggtttt	caaaaataat	tcaacaaaga	aacaatacaa	aaagtgggt	3180
gaatttaccta	tcacatttcc	caatcttgc	tattcagaat	gctgtttatt	tagtgcgtat	3240
gatttagcact	tgattgaaga	ttcttttaaa	atactatcag	ttaaacattt	aatatgatta	3300
tgattaatgt	attcattatg	ctacagaact	gacataagaa	tcaataaaaat	gattgtttt	3360
ctctg						3365

```
<210> 2
<211> 1025
<212> PRT
<213> homo sapiens
```

```

<400> 2
Met Ser Asn Gly Tyr Ser Thr Asp Glu Asn Phe Arg Tyr Leu Ile Ser
 1           5           10           15
Cys Phe Arg Ala Arg Val Lys Met Tyr Ile Gln Val Glu Pro Val Leu
 20          25          30
Asp Tyr Leu Thr Phe Leu Pro Ala Glu Val Lys Glu Gln Ile Gln Arg
 35          40          45
Thr Val Ala Thr Ser Gly Asn Met Gln Ala Val Glu Leu Leu Leu Ser
 50          55          60
Thr Leu Glu Lys Gly Val Trp His Leu Gly Trp Thr Arg Glu Phe Val
 65          70          75          80
Glu Ala Leu Arg Arg Thr Gly Ser Pro Leu Ala Ala Arg Tyr Met Asn
 85          90          95
Pro Glu Leu Thr Asp Leu Pro Ser Pro Ser Phe Glu Asn Ala His Asp
100         105         110
Glu Tyr Leu Gln Leu Leu Asn Leu Leu Gln Pro Thr Leu Val Asp Lys
115         120         125
Leu Leu Val Arg Asp Val Leu Asp Lys Cys Met Glu Glu Glu Leu Leu
130         135         140
Thr Ile Glu Asp Arg Asn Arg Ile Ala Ala Ala Glu Asn Asn Gly Asn

```

145	150	155	160
Glu Ser Gly Val Arg	Glu Leu Leu Lys	Arg Ile Val Gln Lys	Glu Asn
165	170	175	
Trp Phe Ser Ala Phe	Leu Asn Val Leu Arg	Gln Thr Gly Asn	Asn Glu
180	185	190	
Leu Val Gln Glu Leu	Thr Gly Ser Asp Cys	Ser Glu Ser Asn	Ala Glu
195	200	205	
Ile Glu Asn Leu Ser Gln	Val Asp Gly Pro Gln	Val Glu Glu Gln	Leu
210	215	220	
Leu Ser Thr Thr Val Gln	Pro Asn Leu Glu	Lys Glu Val Trp	Gly Met
225	230	235	240
Glu Asn Asn Ser Ser	Glu Ser Ser Phe	Ala Asp Ser Ser	Val Val Ser
245	250	255	
Glu Ser Asp Thr Ser	Leu Ala Glu	Gly Ser Val Ser	Cys Leu Asp Glu
260	265	270	
Ser Leu Gly His Asn	Ser Asn Met	Gly Ser Asp Ser	Gly Thr Met Gly
275	280	285	
Ser Asp Ser Asp	Glu Glu Asn	Val Ala Ala Arg	Ala Ser Pro Glu Pro
290	295	300	
Glu Leu Gln Leu Arg	Pro Tyr Gln	Met Glu Val Ala	Gln Pro Ala Leu
305	310	315	320
Glu Gly Lys Asn Ile	Ile Ile Cys	Leu Pro Thr Gly Ser	Gly Lys Thr
325	330	335	
Arg Val Ala Val Tyr	Ile Ala Lys	Asp His Leu Asp Lys	Lys Lys Lys
340	345	350	
Ala Ser Glu Pro	Gly Lys Val	Ile Val Leu Val Asn	Lys Val Leu Leu
355	360	365	
Val Glu Gln Leu Phe	Arg Lys Glu Phe	Gln Pro Phe Leu	Lys Lys Trp
370	375	380	
Tyr Arg Val Ile Gly	Leu Ser Gly Asp	Thr Gln Leu Lys	Ile Ser Phe
385	390	395	400
Pro Glu Val Val Lys	Ser Cys Asp	Ile Ile Ile Ser	Thr Ala Gln Ile
405	410	415	
Leu Glu Asn Ser	Leu Leu Asn	Leu Glu Asn Gly	Glu Asp Ala Gly Val
420	425	430	
Gln Leu Ser Asp	Phe Ser	Leu Ile Ile Asp	Glu Cys His His Thr
435	440	445	
Asn Lys Glu Ala Val	Tyr Asn Asn Ile	Met Arg His Tyr	Leu Met Gln
450	455	460	
Lys Leu Lys Asn	Asn Arg Leu Lys	Glu Asn Lys Pro	Val Ile Pro
465	470	475	480
Leu Pro Gln Ile	Leu Gly Leu Thr	Ala Ser Pro Gly	Val Gly Gly Ala
485	490	495	
Thr Lys Gln Ala Lys	Ala Glu Glu His	Ile Leu Lys	Leu Cys Ala Asn
500	505	510	
Leu Asp Ala Phe	Thr Ile Lys	Thr Val Lys	Glu Asn Leu Asp Gln Leu
515	520	525	
Lys Asn Gln Ile	Gln Glu Pro	Cys Lys Phe	Ala Ile Ala Asp Ala
530	535	540	
Thr Arg Glu Asp	Pro Phe Lys	Glu Lys Leu	Leu Glu Ile Met Thr Arg
545	550	555	560
Ile Gln Thr Tyr	Cys Gln Met	Ser Pro Met	Ser Asp Phe Gly Thr Gln
565	570	575	
Pro Tyr Glu Gln	Trp Ala Ile	Gln Met Glu	Lys Lys Ala Ala Lys Lys
580	585	590	
Gly Asn Arg Lys	Glu Arg Val	Cys Ala Glu His	Leu Arg Lys Tyr Asn
595	600	605	

Glu Ala Leu Gln Ile Asn Asp Thr Ile Arg Met Ile Asp Ala Tyr Thr
 610 615 620
 His Leu Glu Thr Phe Tyr Asn Glu Glu Lys Asp Lys Lys Phe Ala Val
 625 630 635 640
 Ile Glu Asp Asp Ser Asp Glu Gly Gly Asp Asp Glu Tyr Cys Asp Gly
 645 650 655
 Asp Glu Asp Glu Asp Asp Leu Lys Pro Leu Lys Leu Asp Glu Thr
 660 665 670
 Asp Arg Phe Leu Met Thr Leu Phe Phe Glu Asn Asn Lys Met Leu Lys
 675 680 685
 Arg Leu Ala Glu Asn Pro Glu Tyr Glu Asn Glu Lys Leu Thr Lys Leu
 690 695 700
 Arg Asn Thr Ile Met Glu Gln Tyr Thr Arg Thr Glu Glu Ser Ala Arg
 705 710 715 720
 Gly Ile Ile Phe Thr Lys Thr Arg Gln Ser Ala Tyr Ala Leu Ser Gln
 725 730 735
 Trp Ile Thr Glu Asn Glu Lys Phe Ala Glu Val Gly Val Lys Ala His
 740 745 750
 His Leu Ile Gly Ala Gly His Ser Ser Glu Phe Lys Pro Met Thr Gln
 755 760 765
 Asn Glu Gln Lys Glu Val Ile Ser Lys Phe Arg Thr Gly Lys Ile Asn
 770 775 780
 Leu Leu Ile Ala Thr Thr Val Ala Glu Glu Gly Leu Asp Ile Lys Glu
 785 790 795 800
 Cys Asn Ile Val Ile Arg Tyr Gly Leu Val Thr Asn Glu Ile Ala Met
 805 810 815
 Val Gln Ala Arg Gly Arg Ala Arg Ala Asp Glu Ser Thr Tyr Val Leu
 820 825 830
 Val Ala His Ser Gly Ser Gly Val Ile Glu His Glu Thr Val Asn Asp
 835 840 845
 Phe Arg Glu Lys Met Met Tyr Lys Ala Ile His Cys Val Gln Asn Met
 850 855 860
 Lys Pro Glu Glu Tyr Ala His Lys Ile Leu Glu Leu Gln Met Gln Ser
 865 870 875 880
 Ile Met Glu Lys Lys Met Lys Thr Lys Arg Asn Ile Ala Lys His Tyr
 885 890 895
 Lys Asn Asn Pro Ser Leu Ile Thr Phe Leu Cys Lys Asn Cys Ser Val
 900 905 910
 Leu Ala Cys Ser Gly Glu Asp Ile His Val Ile Glu Lys Met His His
 915 920 925
 Val Asn Met Thr Pro Glu Phe Lys Glu Leu Tyr Ile Val Arg Glu Asn
 930 935 940
 Lys Ala Leu Gln Lys Lys Cys Ala Asp Tyr Gln Ile Asn Gly Glu Ile
 945 950 955 960
 Ile Cys Lys Cys Gly Gln Ala Trp Gly Thr Met Met Val His Lys Gly
 965 970 975
 Leu Asp Leu Pro Cys Leu Lys Ile Arg Asn Phe Val Val Val Phe Lys
 980 985 990
 Asn Asn Ser Thr Lys Lys Gln Tyr Lys Lys Trp Val Glu Leu Pro Ile
 995 1000 1005
 Thr Phe Pro Asn Leu Asp Tyr Ser Glu Cys Cys Leu Phe Ser Asp Glu
 1010 1015 1020
 Asp
 1025

<210> 3
 <211> 1036

<212> DNA
 <213> homo sapiens

 <220>
 <221> misc_feature
 <222> 551
 <223> n = A,T,C or G

 <400> 3
 gcacatttg gcctacaaag gactttattg ttaaggcaga acctgctggg aaaacaaaat 60
 atccgcgga ggagcttgc tttgggtgc agagagaatt cgcttcctt 120
 ttctgtttcc cgccgtgtcc ttaaccaaag gcctccttc ttccacccgccc cccacaaaaa 180
 ggtggcggtcc ccctgaggaa actccctccc cgccaggcag attacgttta caaagtctg 240
 agaagagaat cgaaacagaa accaaagtca ggcaactct gtaagaactg cctgacagaa 300
 agctggactc aaagetccta cccgagtgtc cagcaggatc gcccgggtcc gggaccccg 360
 gcgcacaccc cagactccaa agtgcgcgcg ctgcccccc caccctgcctg cccggggccc 420
 gcgccgcgc cccgtccca cttggccgc tggccacctg cccaggtcg agtgcagccc 480
 cggcgccgg cctgagagcc ctgtggacaa cctcgattt gtcaggcaca gagcggtaga 540
 ccctgttct ntaagtgggc agcggacagc ggcaacgcata ttccacctgt cccgcagaca 600
 acagcaccat ctgctggga gaacccttc cttctctga gaaagaaaaga tgcataatgg 660
 gtattccaca gacgagaatt tccgctatct catctcgatc ttccaggccca gggtaaaaat 720
 gtacatccag gtggagcctg tgctggacta cctgaccttt ctgcctgcag aggtgaagga 780
 gcagattcag aggacagtcg ccaccccccga aacatgcag gcaattgtac tgctgttag 840
 caccttggag aagggagtcg ggcaccccttgg ttggactcgga aatttcgtgg agggccctccg 900
 gagaaccggc agccctctgg ccccccgtca catgaaccct gagctcacgg acttgccttc 960
 tccatcgtt gagaacgctc atgatgaata tctccaactg ctgaaccccttcc ttcagccac 1020
 tctgggtggac aagctt 1036

<210> 4
 <211> 3627
 <212> DNA
 <213> homo sapiens

 <400> 4
 gcgccgcgc ctgagagccc tttggacaac ctgcgttattt tcaggcacag agcggtagac 60
 cctgcttc taagtggca gcccggcagcg gcacgcacat ttccacctgtc cccgacacaa 120
 cagcaccatc tgcttggag aacccttc cttctctgaa aagaaaagat gtcgaatggg 180
 tattccacag acgagaattt cccgtatctc atctcgatc tcaggcccg ggtgaaaatg 240
 tacatccagg tggagcctgt gctggactac ctgacccttc tgcctgcaga ggtgaaggag 300
 cagattcaga ggacagtcgc caccctccggg aacatgcagg cagttgaact gctgctgagc 360
 accttggaga agggagtcg gaccccttggg ttggactcgaa aatttcgtggaa gggccctccgg 420
 agaaccggc gccccttc gcccggcgtac atgaacccttgc agtcacggc cttgccttc 480
 ccatcgttt agaacgctca tgcataatat ctccaaactgc tgaaccccttcc tcaagccact 540
 ctgggtggaca agcttcttagt tagagacgtc ttggataagt gcatggagga ggaactgttg 600
 acaatttgaag acagaaaaccg gattgtctgc gcagaaaaca atggaaaatgtc atcagggtgt 660
 agagagctac taaaaaggat tttggactgtc aaaaactgtt tttctgttgcatt tctgtatgtt 720
 ttccgtcaaa caggaaacaa tgaacttgc caagatgtt caggctctga ttgctcagaa 780
 agcaatgcac agatttggaa ttatccaaat gttgtggcgc ctcaactgttgc agagcaactt 840
 ctttcaacca cagttcagcc aatctggag aaggaggtct gggggatgttgc gaataactca 900
 tcagaatcat cttttgcaga ttcttctgttgc gtttccaaat cagacacacaag tttggcagaa 960
 ggaagtgtca gctgttttgc tggaaagtctt ggacataaca gcaacatggg cagtgttca 1020
 ggcaccatgg gaaagtgttgc agatgttgc aatgtggcgc caagacatc tccggagcc 1080
 gaactccagc tcaggcccttca cccaaatggaa gtttccggc cagcccttggaa agggaaagat 1140
 atcatcatct gcctccctac agggaggtggaa aaaaaccatggc tggctgttttca cattgtcaag 1200
 gatcaacttag acaagaagaa aaaaacatctt gggcctggaa aagtttatgt tcttgcataat 1260
 aaggacttgc tagttgaaca gctttccgc aaggagttcc aaccatgttcaat 1320

```
<210> 5
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 5
gccaccatgt acccatacga cgtcccagac tacgctatgt cgaatgggta ttccacagac 60
g 61

<210> 6
<211> 25
<212> DNA
<213> Artificial Sequence
```

<220>
<223> synthetic oligonucleotide

<400> 6
atgtcgaatg ggtattccac agacg

25

<210> 7
<211> 1025
<212> PRT
<213> homo sapiens

<400> 7
Met Ser Asn Gly Tyr Ser Thr Asp Glu Asn Phe Arg Tyr Leu Ile Ser
1 5 10 15
Cys Phe Arg Ala Arg Val Lys Met Tyr Ile Gln Val Glu Pro Val Leu
20 25 30
Asp Tyr Leu Thr Phe Leu Pro Ala Glu Val Lys Glu Gln Ile Gln Arg
35 40 45
Thr Val Ala Thr Ser Gly Asn Met Gln Ala Val Glu Leu Leu Ser
50 55 60
Thr Leu Glu Lys Gly Val Trp His Leu Gly Trp Thr Arg Glu Phe Val
65 70 75 80
Glu Ala Leu Arg Arg Thr Gly Ser Pro Leu Ala Ala Arg Tyr Met Asn
85 90 95
Pro Glu Leu Thr Asp Leu Pro Ser Pro Ser Phe Glu Asn Ala His Asp
100 105 110
Glu Tyr Leu Gln Leu Leu Asn Leu Leu Gln Pro Thr Leu Val Asp Lys
115 120 125
Leu Leu Val Arg Asp Val Leu Asp Lys Cys Met Glu Glu Glu Leu Leu
130 135 140
Thr Ile Glu Asp Arg Asn Arg Ile Ala Ala Ala Glu Asn Asn Gly Asn
145 150 155 160
Glu Ser Gly Val Arg Glu Leu Leu Lys Arg Ile Val Gln Lys Glu Asn
165 170 175
Trp Phe Ser Ala Phe Leu Asn Val Leu Arg Gln Thr Gly Asn Asn Glu
180 185 190
Leu Val Gln Glu Leu Thr Gly Ser Asp Cys Ser Glu Ser Asn Ala Glu
195 200 205
Ile Glu Asn Leu Ser Gln Val Asp Gly Pro Gln Val Glu Glu Gln Leu
210 215 220
Leu Ser Thr Thr Val Gln Pro Asn Leu Glu Lys Glu Val Trp Gly Met
225 230 235 240
Glu Asn Asn Ser Ser Glu Ser Ser Phe Ala Asp Ser Ser Val Val Ser
245 250 255
Glu Ser Asp Thr Ser Leu Ala Glu Gly Ser Val Ser Cys Leu Asp Glu
260 265 270
Ser Leu Gly His Asn Ser Asn Met Gly Ser Asp Ser Gly Thr Met Gly
275 280 285
Ser Asp Ser Asp Glu Glu Asn Val Ala Ala Arg Ala Ser Pro Glu Pro
290 295 300
Glu Leu Gln Leu Arg Pro Tyr Gln Met Glu Val Ala Gln Pro Ala Leu
305 310 315 320
Glu Gly Lys Asn Ile Ile Ile Cys Leu Pro Thr Gly Ser Gly Lys Thr
325 330 335
Arg Val Ala Val Tyr Ile Ala Lys Asp His Leu Asp Lys Lys Lys Lys
340 345 350
Ala Ser Glu Pro Gly Lys Val Ile Val Leu Val Asn Lys Val Leu Leu

355	360	365	
Val Glu Gln Leu Phe Arg Lys	Glu Phe Gln Pro Phe Leu Lys Lys Trp		
370	375	380	
Tyr Arg Val Ile Gly Leu Ser Gly Asp Thr	Gln Leu Lys Ile Ser Phe		
385	390	395	400
Pro Glu Val Val Lys Ser Cys Asp Ile Ile	Ile Ser Thr Ala Gln Ile		
405	410	415	
Leu Glu Asn Ser Leu Leu Asn Leu Glu Asn Gly	Glu Asp Ala Gly Val		
420	425	430	
Gln Leu Ser Asp Phe Ser Leu Ile Ile Asp	Glu Cys His His Thr		
435	440	445	
Asn Lys Glu Ala Val Tyr Asn Asn Ile Met	Arg His Tyr Leu Met Gln		
450	455	460	
Lys Leu Lys Asn Asn Arg	Leu Lys Lys Glu Asn Lys Pro Val Ile Pro		
465	470	475	480
Leu Pro Gln Ile Leu Gly Leu Thr Ala Ser	Pro Gly Val Gly Gly Ala		
485	490	495	
Thr Lys Gln Ala Lys Ala Glu Glu His Ile	Leu Lys Leu Cys Ala Asn		
500	505	510	
Leu Asp Ala Phe Thr Ile Lys Thr Val	Lys Glu Asn Leu Asp Gln Leu		
515	520	525	
Lys Asn Gln Ile Gln Glu Pro Cys Lys Lys	Phe Ala Ile Ala Asp Ala		
530	535	540	
Thr Arg Glu Asp Pro Phe Lys Glu Lys Leu	Glu Ile Met Thr Arg		
545	550	555	560
Ile Gln Thr Tyr Cys Gln Met Ser Pro	Met Ser Asp Phe Gly Thr Gln		
565	570	575	
Pro Tyr Glu Gln Trp Ala Ile Gln Met Glu	Lys Lys Ala Ala Lys Glu		
580	585	590	
Gly Asn Arg Lys Glu Arg Val Cys Ala Glu	His Leu Arg Lys Tyr Asn		
595	600	605	
Glu Ala Leu Gln Ile Asn Asp Thr Ile Arg	Met Ile Asp Ala Tyr Thr		
610	615	620	
His Leu Glu Thr Phe Tyr Asn Glu Glu Lys	Asp Lys Phe Ala Val		
625	630	635	640
Ile Glu Asp Asp Ser Asp Glu Gly Gly Asp	Asp Glu Tyr Cys Asp Gly		
645	650	655	
Asp Glu Asp Glu Asp Asp Leu Lys Lys	Pro Leu Lys Leu Asp Glu Thr		
660	665	670	
Asp Arg Phe Leu Met Thr Leu Phe Phe Glu	Asn Asn Lys Met Leu Lys		
675	680	685	
Arg Leu Ala Glu Asn Pro Glu Tyr Glu Asn	Glu Lys Leu Thr Lys Leu		
690	695	700	
Arg Asn Thr Ile Met Glu Gln Tyr Thr Arg	Thr Glu Ser Ala Arg		
705	710	715	720
Gly Ile Ile Phe Thr Lys Thr Arg Gln Ser	Ala Tyr Ala Leu Ser Gln		
725	730	735	
Trp Ile Thr Glu Asn Glu Lys Phe Ala Glu	Val Gly Val Lys Ala His		
740	745	750	
His Leu Ile Gly Ala Gly His Ser Ser Glu	Phe Lys Pro Met Thr Gln		
755	760	765	
Asn Glu Gln Lys Glu Val Ile Ser Lys Phe	Arg Thr Gly Lys Ile Asn		
770	775	780	
Leu Leu Ile Ala Thr Thr Val Ala Glu Glu	Gly Leu Asp Ile Lys Glu		
785	790	795	800
Cys Asn Ile Val Ile Arg Tyr Gly Leu Val	Thr Asn Glu Ile Ala Met		
805	810	815	

Val Gln Ala Arg Gly Arg Ala Arg Ala Asp Glu Ser Thr Tyr Val Leu
 820 825 830
 Val Ala His Ser Gly Ser Gly Val Ile Glu Arg Glu Thr Val Asn Asp
 835 840 845
 Phe Arg Glu Lys Met Met Tyr Lys Ala Ile His Cys Val Gln Asn Met
 850 855 860
 Lys Pro Glu Glu Tyr Ala His Lys Ile Leu Glu Leu Gln Met Gln Ser
 865 870 875 880
 Ile Met Glu Lys Lys Met Lys Thr Lys Arg Asn Ile Ala Lys His Tyr
 885 890 895
 Lys Asn Asn Pro Ser Leu Ile Thr Phe Leu Cys Lys Asn Cys Ser Val
 900 905 910
 Leu Ala Cys Ser Gly Glu Asp Ile His Val Ile Glu Lys Met His His
 915 920 925
 Val Asn Met Thr Pro Glu Phe Lys Glu Leu Tyr Ile Val Arg Glu Asn
 930 935 940
 Lys Ala Leu Gln Lys Lys Cys Ala Asp Tyr Gln Ile Asn Gly Glu Ile
 945 950 955 960
 Ile Cys Lys Cys Gly Gln Ala Trp Gly Thr Met Met Val His Lys Gly
 965 970 975
 Leu Asp Leu Pro Cys Leu Lys Ile Arg Asn Phe Val Val Val Phe Lys
 980 985 990
 Asn Asn Ser Thr Lys Lys Gln Tyr Lys Lys Trp Val Glu Leu Pro Ile
 995 1000 1005
 Thr Phe Pro Asn Leu Asp Tyr Ser Glu Cys Cys Leu Phe Ser Asp Glu
 1010 1015 1020
 Asp
 1025

<210> 8
 <211> 3365
 <212> DNA
 <213> homo sapiens

<400> 8
 gcgccgcggc ctgagagccc tgtggacaac ctcgtcattt tcagggcacag agcggttagac 60
 cctgcttctc taagtggca gcggacagcg gcacgcacat ttcacctgtc ccgcagacaa 120
 cagcaccatc tgcttggag aaccctctcc cttctctgag aaagaaaagat gtcgaatggg 180
 tattccacag acgagaattt ccgctatctc atctcggtc tcagggccag ggtgaaaatg 240
 tacatccagg tggagctgt gctggactac ctgacccttc tgccctgcaga ggtgaaggag 300
 cagattcaga ggacagtcgc cacccggg aacatgcagg cagttgaact gctgctgagc 360
 accttggaga agggagtctg gcaccttggg tggactcggg aattcgtgga gcccctccgg 420
 agaaccggca gccccttggc cggccgtac atgaaccctg agctcacggc cttgcctct 480
 ccatcggttt agaacgcgtca tgatgaataat ctccaactgc tgaacacct tcagccact 540
 ctgggtggaca agcttctagt tagagacgtc ttggataagt gcatggagga ggaactgttg 600
 acaatttgaag acagaaaaccg gattgtctc gcagaaaaaca atggaaaatga atcaggtgt 660
 agagagctac taaaaaggat tgtcagaaa gaaaactgtt tctctgtcatt tctgaatgtt 720
 cttcgtcaaa cagaaaaaca tgaacttgc caagagttt caggctctga ttgctcagaa 780
 agcaatgcgtc agattggaaa tttatcacaat gttgatggtc ctcagaatggc agagcaactt 840
 ctttcaacca cagttcagcc aaatctggag aaggaggtct ggggcatggc gaataactca 900
 tcagaatcat cttttcaga ttcttctgtt gtttcagaat cagacacacaag tttggcagaa 960
 ggaagtgtca gctgcttgc tgaaagtctt ggacataaca gcaacatggg cagtgattca 1020
 ggcaccatgg gaagtggattc agatgaagag aatgtggcag caagagcatc cccggagcca 1080
 gaactccagc tcaggcctta ccaaattggaa gttgcccagc cagccttggc agggaaagat 1140
 atcatcatct gcctccctac agggagtggc aaaaccagag tggctgttta cattgccaag 1200
 gatcacttag acaagaagaa aaaagcatct gagcctggaa aagttatagt tcttgcataat 1260

aaggtaactgc tagttgaaca gctttccgc aaggagttcc aaccatttt gaagaaatgg 1320
 tatcggttta ttggattaag tggtgatacc caactgaaaa tatcatttc agaagttgtc 1380
 aagtccctgtg atattattat cagtagct caaatcctt aaaaactccct cttaaacttg 1440
 gaaaatggag aagatgctgg tggtaattt tcagacttt ccctcattat cattgtgaa 1500
 tgtcatcaca ccaacaaaga agcagtgtat aataacatca tgaggcatta tttgatgcag 1560
 aagttgaaaa acaatagact caagaaagaa aacaaaccag tgattccct tcctcagata 1620
 ctgggactaa cagcttcacc tgggtttgaa ggggccccga agcaagccaa agctgaagaa 1680
 cacatTTaa aactatgtgc caatcttgcat gcatttacta taaaactgt taaagaaaaac 1740
 cttgatcaac tgaaaaacc aatacaggag ccatgcaga agtttgcatt tgcatgtc 1800
 accagagaag atccattaa agagaaactt ctgaaataa tgacaaggat tcaaacttat 1860
 tgtcaatgtg gtccaatgtc agattttgaa actcaaccct atgaacaatg ggcattcaa 1920
 atggaaaaaa aagctgcaaa agaaggaaat cgccaaagaac gtgttgc 1980
 aggaagtaca atgaggccct acaaattat gacacaattt gaaatgataga tgcgtatact 2040
 catcttgaaa ctttctataa tgaagagaaa gataagaatg ttgcgtcat agaagatgat 2100
 agtcatgagg gtgggtatgtg tgatgtt gatggatg aagatgagga tgatttaaag 2160
 aaaccttga aactggatgaa aacagataga tttctcatga ctttatttt tgaaaacaat 2220
 aaaatgttga aaaggctggc tgaaaaccca gaatatgaaa atgaaaagct gaccaattt 2280
 agaaatacca taatggagca atatactagg actgaggaat cgcacggg aataatctt 2340
 acaaaaaacac gacagagtgc atatgcgtt tccctgtgaa ttactgaaaaa tgaaaattt 2400
 gctgaagtag gagtciaaagc ccacatctg attggagctg gacacagcag tgagttcaaa 2460
 cccatgacac agaatgaca aaaagaagtc atttagataat ttgcactgg aaaaataat 2520
 ctgcttatcg ctaccacatg ggcagaagaa ggtctggata taaaagaatg taacatgtt 2580
 atccgttatg gtctcggtcac caatgaaata gccatgttcc agggccgtgg tcgagccaga 2640
 gctgtatgaga gcacccatgt cctgggtgtc cacatgtt caggagttt cgaacatgag 2700
 acagttatg atttccgaga gaagatgatg tataaagcta tacattgtt tcaaaatatg 2760
 aaaccagagg agtatgtca taagatttt gaattacaga tgcaaagat aatggaaaag 2820
 aaaatgaaaaa ccaagagaaa tattgccaag cattacaaga ataaccatc actaataact 2880
 ttccttgc aaaaactgcag tggcttagcc tggctgggg aagatatcca tgtaattgag 2940
 aaaatgcac acgtcaatgat gaccccgaaa ttcaaggaac ttacattgt aagagaaaac 3000
 aaagcactgc aaaagaatg tgccgactat caaataatg gtgaaatcat ctgcaatgt 3060
 ggcaggctt gggacaat gatggcgtc aaaggcttag attgccttg tctcaaaaata 3120
 aggaatttt tagtggttt caaaaataat tcaacaaaga aacaatacaa aaagtggta 3180
 gaattaccta tcacatttcc caatcttgcattt cttttttttt tagtcatgag 3240
 gattagcact tgattgaaga ttctttttaaa atactatcg ttaaacattt aatatgatta 3300
 tgattatgt attcattatg ctacagaact gacataagaa tcaataaaaat gattgttta 3360
 ctctg 3365

<210> 9
 <211> 1025
 <212> PRT
 <213> homo sapiens

<400> 9
 Met Ser Asn Gly Tyr Ser Thr Asp Glu Asn Phe Arg Tyr Leu Ile Ser
 1 5 10 15
 Cys Phe Arg Ala Arg Val Lys Met Tyr Ile Gln Val Glu Pro Val Leu
 20 25 30
 Asp Tyr Leu Thr Phe Leu Pro Ala Glu Val Lys Glu Gln Ile Gln Arg
 35 40 45
 Thr Val Ala Thr Ser Gly Asn Met Gln Ala Val Glu Leu Leu Leu Ser
 50 55 60
 Thr Leu Glu Lys Gly Val Trp His Leu Gly Trp Thr Arg Glu Phe Val
 65 70 75 80
 Glu Ala Leu Arg Arg Thr Gly Ser Pro Leu Ala Ala Arg Tyr Met Asn
 85 90 95
 Pro Glu Leu Thr Asp Leu Pro Ser Pro Ser Phe Glu Asn Ala His Asp
 100 105 110

Glu Tyr Leu Gln Leu Leu Asn Leu Leu Gln Pro Thr Leu Val Asp Lys
115 120 125
Leu Leu Val Arg Asp Val Leu Asp Lys Cys Met Glu Glu Glu Leu Leu
130 135 140
Thr Ile Glu Asp Arg Asn Arg Ile Ala Ala Ala Glu Asn Asn Gly Asn
145 150 155 160
Glu Ser Gly Val Arg Glu Leu Leu Lys Arg Ile Val Gln Lys Glu Asn
165 170 175
Trp Phe Ser Ala Phe Leu Asn Val Leu Arg Gln Thr Gly Asn Asn Glu
180 185 190
Leu Val Gln Glu Leu Thr Gly Ser Asp Cys Ser Glu Ser Asn Ala Glu
195 200 205
Ile Glu Asn Leu Ser Gln Val Asp Gly Pro Gln Val Glu Glu Gln Leu
210 215 220
Leu Ser Thr Thr Val Gln Pro Asn Leu Glu Lys Glu Val Trp Gly Met
225 230 235 240
Glu Asn Asn Ser Ser Glu Ser Ser Phe Ala Asp Ser Ser Val Val Ser
245 250 255
Glu Ser Asp Thr Ser Leu Ala Glu Gly Ser Val Ser Cys Leu Asp Glu
260 265 270
Ser Leu Gly His Asn Ser Asn Met Gly Ser Asp Ser Gly Thr Met Gly
275 280 285
Ser Asp Ser Asp Glu Glu Asn Val Ala Ala Arg Ala Ser Pro Glu Pro
290 295 300
Glu Leu Gln Leu Arg Pro Tyr Gln Met Glu Val Ala Gln Pro Ala Leu
305 310 315 320
Glu Gly Lys Asn Ile Ile Ile Cys Leu Pro Thr Gly Ser Gly Lys Thr
325 330 335
Arg Val Ala Val Tyr Ile Ala Lys Asp His Leu Asp Lys Lys Lys
340 345 350
Ala Ser Glu Pro Gly Lys Val Ile Val Leu Val Asn Lys Val Leu Leu
355 360 365
Val Glu Gln Leu Phe Arg Lys Glu Phe Gln Pro Phe Leu Lys Lys Trp
370 375 380
Tyr Arg Val Ile Gly Leu Ser Gly Asp Thr Gln Leu Lys Ile Ser Phe
385 390 395 400
Pro Glu Val Val Lys Ser Cys Asp Ile Ile Ile Ser Thr Ala Gln Ile
405 410 415
Leu Glu Asn Ser Leu Leu Asn Leu Glu Asn Gly Glu Asp Ala Gly Val
420 425 430
Gln Leu Ser Asp Phe Ser Leu Ile Ile Ile Asp Glu Cys His His Thr
435 440 445
Asn Lys Glu Ala Val Tyr Asn Asn Ile Met Arg His Tyr Leu Met Gln
450 455 460
Lys Leu Lys Asn Asn Arg Leu Lys Lys Glu Asn Lys Pro Val Ile Pro
465 470 475 480
Leu Pro Gln Ile Leu Gly Leu Thr Ala Ser Pro Gly Val Gly Ala
485 490 495
Thr Lys Gln Ala Lys Ala Glu Glu His Ile Leu Lys Leu Cys Ala Asn
500 505 510
Leu Asp Ala Phe Thr Ile Lys Thr Val Lys Glu Asn Leu Asp Gln Leu
515 520 525
Lys Asn Gln Ile Gln Glu Pro Cys Lys Lys Phe Ala Ile Ala Asp Ala
530 535 540
Thr Arg Glu Asp Pro Phe Lys Glu Lys Leu Leu Glu Ile Met Thr Arg
545 550 555 560
Ile Gln Thr Tyr Cys Gln Met Ser Pro Met Ser Asp Phe Gly Thr Gln

565	570	575	
Pro Tyr Glu Gln Trp Ala Ile Gln Met	Glu Lys Lys Ala Ala Lys Glu		
580	585	590	
Gly Asn Arg Lys Glu Arg Val Cys Ala Glu His Leu Arg Lys Tyr Asn			
595	600	605	
Glu Ala Leu Gln Ile Asn Asp Thr Ile Arg Met Ile Asp Ala Tyr Thr			
610	615	620	
His Leu Glu Thr Phe Tyr Asn Glu Glu Lys Asp Lys Lys Phe Ala Val			
625	630	635	640
Ile Glu Asp Asp Ser Asp Glu Gly Gly Asp Asp Glu Tyr Cys Asp Gly			
645	650	655	
Asp Glu Asp Glu Asp Asp Leu Lys Lys Pro Leu Lys Leu Asp Glu Thr			
660	665	670	
Asp Arg Phe Leu Met Thr Leu Phe Glu Asn Asn Lys Met Leu Lys			
675	680	685	
Arg Leu Ala Glu Asn Pro Glu Tyr Glu Asn Glu Lys Leu Thr Lys Leu			
690	695	700	
Arg Asn Thr Ile Met Glu Gln Tyr Thr Arg Thr Glu Glu Ser Ala Arg			
705	710	715	720
Gly Ile Ile Phe Thr Lys Thr Arg Gln Ser Ala Tyr Ala Leu Ser Gln			
725	730	735	
Trp Ile Thr Glu Asn Glu Lys Phe Ala Glu Val Gly Val Lys Ala His			
740	745	750	
His Leu Ile Gly Ala Gly His Ser Ser Glu Phe Lys Pro Met Thr Gln			
755	760	765	
Asn Glu Gln Lys Glu Val Ile Ser Lys Phe Arg Thr Gly Lys Ile Asn			
770	775	780	
Leu Leu Ile Ala Thr Thr Val Ala Glu Glu Gly Leu Asp Ile Lys Glu			
785	790	795	800
Cys Asn Ile Val Ile Arg Tyr Gly Leu Val Thr Asn Glu Ile Ala Met			
805	810	815	
Val Gln Ala Arg Gly Arg Ala Arg Ala Asp Glu Ser Thr Tyr Val Leu			
820	825	830	
Val Ala His Ser Gly Ser Gly Val Ile Glu His Glu Thr Val Asn Asp			
835	840	845	
Phe Arg Glu Lys Met Met Tyr Lys Ala Ile His Cys Val Gln Asn Met			
850	855	860	
Lys Pro Glu Glu Tyr Ala His Lys Ile Leu Glu Leu Gln Met Gln Ser			
865	870	875	880
Ile Met Glu Lys Lys Met Lys Thr Lys Arg Asn Ile Ala Lys His Tyr			
885	890	895	
Lys Asn Asn Pro Ser Leu Ile Thr Phe Leu Cys Lys Asn Cys Ser Val			
900	905	910	
Leu Ala Cys Ser Gly Glu Asp Ile His Val Ile Glu Lys Met His His			
915	920	925	
Val Asn Met Thr Pro Glu Phe Lys Glu Leu Tyr Ile Val Arg Glu Asn			
930	935	940	
Lys Ala Leu Gln Lys Lys Cys Ala Asp Tyr Gln Ile Asn Gly Glu Ile			
945	950	955	960
Ile Cys Lys Cys Gly Gln Ala Trp Gly Thr Met Met Val His Lys Gly			
965	970	975	
Leu Asp Leu Pro Cys Leu Lys Ile Arg Asn Phe Val Val Val Phe Lys			
980	985	990	
Asn Asn Ser Thr Lys Lys Gln Tyr Lys Lys Trp Val Glu Leu Pro Ile			
995	1000	1005	
Thr Phe Pro Asn Leu Asp Tyr Ser Glu Cys Cys Leu Phe Ser Asp Glu			
1010	1015	1020	

Asp
1025

<210> 10
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 10
tcactaatcc tcatcactaa ataaacagc 29

<210> 11
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 11
ttttttttt ttcagagtaa aacaatc 27

<210> 12
<211> 486
<212> PRT
<213> homo sapiens

<400> 12
Met Glu Leu Arg Ser Tyr Gln Trp Glu Val Ile Met Pro Ala Leu Glu
1 5 10 15
Gly Lys Asn Ile Ile Ile Trp Leu Pro Thr Gly Ala Gly Lys Thr Arg
20 25 30
Ala Ala Ala Tyr Val Ala Lys Arg His Leu Glu Thr Val Asp Gly Ala
35 40 45
Lys Val Val Val Leu Val Asn Arg Val His Leu Val Thr Gln His Gly
50 55 60
Glu Glu Phe Arg Arg Met Leu Asp Gly Arg Trp Thr Val Thr Thr Leu
65 70 75 80
Ser Gly Asp Met Gly Pro Arg Ala Gly Phe Gly His Leu Ala Arg Cys
85 90 95
His Asp Leu Leu Ile Cys Thr Ala Glu Leu Leu Gln Met Ala Leu Thr
100 105 110
Ser Pro Glu Glu Glu His Val Glu Leu Thr Val Phe Ser Leu Ile
115 120 125
Val Val Asp Glu Cys His His Thr His Lys Asp Thr Val Tyr Asn Val
130 135 140
Ile Met Ser Gln Tyr Leu Glu Leu Lys Leu Gln Arg Ala Gln Pro Leu
145 150 155 160
Pro Gln Val Leu Gly Leu Thr Ala Ser Pro Gly Thr Gly Gly Ala Ser
165 170 175
Lys Leu Asp Gly Ala Ile Asn His Val Leu Gln Leu Cys Ala Asn Leu
180 185 190
Asp Thr Trp Cys Ile Met Ser Pro Gln Asn Cys Cys Pro Gln Leu Gln

195	200	205	
Glu His Ser Gln Gln Pro Cys Lys Gln Tyr Asn Leu Cys His Arg Arg			
210	215	220	
Ser Gln Asp Pro Phe Gly Asp Leu Leu Lys Lys Leu Met Asp Gln Ile			
225	230	235	240
His Asp His Leu Glu Met Pro Glu Leu Ser Arg Lys Phe Gly Thr Gln			
245	250	255	
Met Tyr Glu Gln Gln Val Val Lys Leu Ser Glu Ala Ala Ala Leu Ala			
260	265	270	
Gly Leu Gln Glu Gln Arg Val Tyr Ala Leu His Leu Arg Arg Tyr Asn			
275	280	285	
Asp Ala Leu Leu Ile His Asp Thr Val Arg Ala Val Asp Ala Leu Ala			
290	295	300	
Ala Leu Gln Asp Phe Tyr His Arg Glu His Val Thr Lys Thr Gln Ile			
305	310	315	320
Leu Cys Ala Glu Arg Arg Leu Leu Ala Leu Phe Asp Asp Arg Lys Asn			
325	330	335	
Glu Leu Ala His Leu Ala Thr His Gly Pro Glu Asn Pro Lys Leu Glu			
340	345	350	
Met Leu Glu Lys Ile Leu Gln Arg Gln Phe Ser Ser Ser Asn Ser Pro			
355	360	365	
Arg Gly Ile Ile Phe Thr Arg Thr Arg Gln Ser Ala His Ser Leu Leu			
370	375	380	
Leu Trp Leu Gln Gln Gln Gly Leu Gln Thr Val Asp Ile Arg Ala			
385	390	395	400
Gln Leu Leu Ile Gly Ala Gly Asn Ser Ser Gln Ser Thr His Met Thr			
405	410	415	
Gln Arg Asp Gln Gln Glu Val Ile Gln Lys Phe Gln Asp Gly Thr Leu			
420	425	430	
Asn Leu Leu Val Ala Thr Ser Val Ala Glu Glu Gly Leu Asp Ile Pro			
435	440	445	
His Cys Asn Val Val Val Arg Tyr Gly Leu Leu Thr Asn Glu Ile Ser			
450	455	460	
Met Val Gln Ala Arg Gly Arg Ala Trp Ala Asp Gln Ser Val Tyr Ala			
465	470	475	480
Phe Val Ala Thr Glu Gly			
485			

<210> 13
 <211> 514
 <212> PRT
 <213> sus scrofa

<400> 13			
His Thr Tyr Ser Pro Leu Lys Pro Arg Lys Tyr Gln Leu Glu Leu Ala			
1	5	10	15
Leu Pro Ala Gln Asn Gly Lys Asn Thr Ile Ile Cys Ala Pro Thr Gly			
20	25	30	
Cys Gly Lys Thr Phe Val Ser Leu Leu Ile Cys Glu His His Leu Lys			
35	40	45	
Lys Phe Pro Arg Gly Arg Lys Gly Lys Val Val Phe Phe Ala Ile Gln			
50	55	60	
Leu Pro Val Tyr Glu Gln Gln Lys Ser Val Phe Ser Lys His Phe Glu			
65	70	75	80
Arg Leu Gly Tyr Lys Val Ala Gly Ile Ser Gly Ala Thr Ser Asp Thr			
85	90	95	

Val Cys Val Glu Gln Ile Val Glu Asn Ser Asp Ile Ile Ile Leu Thr
 100 105 110
 Pro Gln Ile Leu Val Asn Cys Leu Thr Asn Gly Thr Ile Pro Ser Leu
 115 120 125
 Ser Val Phe Thr Leu Met Ile Phe Asp Glu Cys His Asn Thr Ser Lys
 130 135 140
 Gln His Pro Tyr Asn Val Ile Met Phe Ser Tyr Leu Asp Arg Lys Leu
 145 150 155 160
 Gly Gly Ser Ser Asp Ser Leu Pro Gln Val Ile Gly Leu Thr Ala Ser
 165 170 175
 Val Gly Val Gly Asp Ala Lys Asn Lys Ala Glu Ala Thr Glu Tyr Ile
 180 185 190
 Cys Lys Leu Cys Ala Ser Leu Asp Thr Ser Val Ile Ala Thr Val Arg
 195 200 205
 Asp Asn Leu Glu Leu Glu Val Val Tyr Lys Pro Gln Lys Phe
 210 215 220
 Phe Arg Lys Val Glu Leu Arg Thr Thr Asp Arg Phe Lys Cys Ile Ile
 225 230 235 240
 Ser Gln Leu Met Met Glu Ile Glu Ser Leu Ala Lys Ser Ile Phe Glu
 245 250 255
 Glu Leu Gly Thr Ile Thr Leu Gly Gly Leu Phe Gln Ile Gln Asn Ser
 260 265 270
 Asn Phe Gly Thr Gln Lys Tyr Glu Gln Trp Ile Val Lys Val Gln Lys
 275 280 285
 Glu Cys Ala Val Phe Gln Met Pro Asp Lys Asp Lys Glu Ser Arg Ile
 290 295 300
 Cys Lys Ala Leu Phe Ser Tyr Met Ser His Leu Arg Ile Tyr Asn Asp
 305 310 315 320
 Ala Leu Ile Ile Asn Glu His Ala Arg Met Lys Asp Ala Leu Asp Tyr
 325 330 335
 Leu Lys Asp Phe Phe Arg Asn Ile Arg Ala Ala Gly Phe Asp Glu Ile
 340 345 350
 Glu Gln Asp Leu Thr Gln Arg Phe Glu Glu Lys Leu Gln Glu Leu Glu
 355 360 365
 Ser Ile Ser Ile Asp Pro Ser Asn Glu Asn Pro Lys Leu Arg Asp Leu
 370 375 380
 Cys Phe Ile Leu Gln Glu Glu Tyr His Leu Asn Pro Glu Thr Arg Thr
 385 390 395 400
 Ile Leu Phe Val Lys Thr Arg Ala Leu Val Asp Ala Leu Lys Lys Trp
 405 410 415
 Ile Lys Glu Asn Pro Lys Leu Ser Phe Leu Lys Pro Ser Ile Leu Thr
 420 425 430
 Gly Arg Gly Lys Thr Asn Gln Asn Ile Gly Met Thr Leu Pro Ala Gln
 435 440 445
 Lys Cys Val Leu Asp Thr Phe Arg Thr Asp Lys Asp Asn Lys Ile Leu
 450 455 460
 Ile Thr Thr Ser Val Ala Asp Glu Gly Ile Asp Ile Ala Gln Cys Asn
 465 470 475 480
 Leu Val Ile Leu Tyr Glu Tyr Val Gly Asn Val Ile Lys Met Ile Gln
 485 490 495
 Thr Arg Gly Arg Gly Arg Ala Arg Gly Ser Lys Cys Phe Leu Leu Thr
 500 505 510
 Ala Asn

<211> 416
<212> PRT
<213> homo sapiens

<400> 14
Asn Leu Tyr Ser Pro Phe Lys Pro Arg Asn Tyr Gln Leu Glu Leu Ala
1 5 10 15
Leu Pro Ala Met Lys Gly Lys Asn Thr Ile Ile Cys Ala Pro Thr Gly
20 25 30
Cys Phe Lys Thr Phe Val Ser Leu Leu Ile Cys Glu His His Leu Lys
35 40 45
Lys Phe Pro Gln Gly Gln Lys Gly Lys Val Val Phe Phe Ala Asn Gln
50 55 60
Ile Pro Val Tyr Glu Gln Lys Ser Val Phe Ser Lys Tyr Phe Glu
65 70 75 80
Arg His Gly Tyr Arg Val Thr Gly Ile Ser Gly Ala Thr Ala Glu Asn
85 90 95
Val Pro Val Glu Gln Ile Val Glu Asn Asn Asp Ile Ile Leu Thr
100 105 110
Pro Gln Ile Leu Val Asn Asn Leu Lys Lys Gly Thr Ile Pro Ser Leu
115 120 125
Ser Ile Phe Thr Leu Met Ile Phe Asp Glu Cys His Asn Thr Ser Lys
130 135 140
Gln His Pro Tyr Asn Met Ile Met Phe Asn Tyr Leu Asp Gln Lys Leu
145 150 155 160
Gly Gly Ser Ser Gly Pro Leu Pro Gln Val Ile Gly Leu Thr Ala Ser
165 170 175
Val Gly Val Gly Asp Ala Lys Asn Thr Asp Glu Ala Leu Asp Tyr Ile
180 185 190
Cys Lys Leu Cys Ala Ser Val Ile Ala Thr Val Lys His Asn Leu Glu
195 200 205
Glu Leu Glu Gln Val Val Tyr Lys Pro Gln Lys Phe Phe Arg Lys Val
210 215 220
Glu Ser Arg Ile Ser Asp Lys Phe Lys Tyr Ile Ile Ala Gln Leu Met
225 230 235 240
Arg Asp Thr Glu Ser Leu Ala Lys Arg Ile Cys Lys Asp Leu Glu Asn
245 250 255
Leu Ser Gln Ile Gln Asn Arg Glu Lys Leu Gln Glu Leu Glu Ser Val
260 265 270
Ser Arg Asp Pro Ser Asn Glu Asn Pro Lys Leu Glu Asp Leu Cys Phe
275 280 285
Ile Leu Gln Glu Glu Tyr His Leu Asn Pro Glu Thr Ile Thr Ile Leu
290 295 300
Phe Val Lys Thr Arg Ala Leu Val Asp Ala Leu Lys Asn Trp Ile Glu
305 310 315 320
Gly Asn Pro Lys Leu Ser Phe Leu Lys Pro Gly Ile Leu Thr Gly Arg
325 330 335
Gly Lys Thr Asn Gln Asn Thr Gly Met Thr Leu Pro Ala Gln Lys Cys
340 345 350
Ile Leu Asp Ala Phe Lys Ala Ser Gly Asp His Asn Ile Leu Ile Ala
355 360 365
Thr Ser Val Ala Asp Glu Gly Ile Asp Ile Ala Gln Cys Asn Leu Val
370 375 380
Ile Leu Tyr Glu Tyr Val Gly Asn Val Ile Lys Met Ile Gln Thr Arg
385 390 395 400
Gly Arg Gly Arg Ala Arg Gly Ser Lys Cys Phe Leu Leu Thr Ser Asn
405 410 415

<210> 15
<211> 503
<212> PRT
<213> *caenorhabditis elegans*

<400> 15
Ala Asp Leu Gln Cys Phe Asn Pro Arg Asp Tyr Gln Val Glu Leu Leu
1 5 10 15
Asp Lys Ala Thr Lys Lys Asn Thr Ile Val Gln Leu Gly Thr Gly Ser
20 25 30
Gly Lys Thr Phe Ile Ala Val Leu Leu Lys Glu Tyr Gly Val Gln
35 40 45
Leu Phe Ala Pro Leu Asp Gln Gly Gly Lys Arg Ala Phe Phe Val Val
50 55 60
Glu Lys Val Asn Leu Val Glu Gln Gln Ala Ile His Ile Glu Val His
65 70 75 80
Thr Ser Phe Lys Val Gly Gln Val His Gly Gln Thr Ser Ser Gly Leu
85 90 95
Trp Asp Ser Lys Glu Gln Cys Asp Gln Phe Met Lys Arg His His Val
100 105 110
Val Val Ile Thr Ala Gln Cys Leu Leu Asp Leu Ile Arg His Ala Tyr
115 120 125
Leu Lys Ile Glu Asp Met Cys Val Leu Ile Phe Asp Glu Cys His His
130 135 140
Ala Leu Gly Ser Gln His Pro Tyr Arg Ser Ile Met Val Asp Tyr Lys
145 150 155 160
Leu Leu Lys Asp Lys Pro Val Pro Arg Val Leu Gly Leu Thr Ala
165 170 175
Ser Leu Ile Lys Ala Lys Val Ala Pro Glu Lys Leu Met Glu Gln Leu
180 185 190
Lys Lys Leu Glu Ser Ala Met Asp Ser Val Ile Glu Thr Ala Ser Asp
195 200 205
Leu Val Ser Leu Ser Lys Tyr Gly Ala Lys Pro Tyr Glu Val Val Ile
210 215 220
Ile Cys Lys Asp Phe Glu Ile Gly Cys Leu Gly Ile Pro Asn Phe Asp
225 230 235 240
Thr Val Ile Glu Ile Phe Asp Glu Thr Val Ala Phe Val Asn Thr Thr
245 250 255
Thr Glu Phe His Pro Asp Leu Asp Leu Asp Pro Arg Arg Pro Ile Lys
260 265 270
Asp Ser Leu Lys Thr Thr Arg Ala Val Phe Arg Gln Leu Gly Pro Trp
275 280 285
Ala Ala Trp Arg Thr Ala Gln Val Trp Glu Lys Glu Leu Gly Lys Ile
290 295 300
Ile Lys Ser Gln Val Leu Pro Asp Lys Thr Leu Arg Phe Leu Asn Met
305 310 315 320
Ala Lys Thr Ser Met Ile Thr Ile Lys Arg Leu Leu Glu Pro Glu Met
325 330 335
Lys Lys Ile Lys Ser Ile Glu Ala Leu Arg Pro Tyr Val Pro Gln Arg
340 345 350
Val Ile Arg Leu Phe Glu Ile Leu Glu Thr Phe Asn Pro Glu Phe Gln
355 360 365
Lys Glu Arg Met Lys Leu Glu Lys Ala Glu His Leu Ser Ala Ile Ile
370 375 380
Phe Val Asp Gln Arg Tyr Ile Ala Tyr Ser Leu Leu Met Met Arg

385	390	395	400
His Ile Lys Ser Trp Glu Pro Lys Phe Lys		Phe Val Asn Pro Asp Tyr	
405		410	415
Val Val Gly Ala Ser Gly Arg Asn Leu Ala Ser Ser Asp Ser Gln Gly			
420		425	430
Leu His Lys Arg Gln Thr Glu Val Leu Arg Arg Phe His Arg Asn Glu			
435		440	445
Ile Asn Cys Leu Ile Ala Thr Ser Val Leu Glu Glu Gly Val Asp Val			
450		455	460
Lys Gln Cys Asn Leu Val Ile Lys Phe Asp Arg Pro Leu Asp Met Arg			
465		470	475
Ser Tyr Val Gln Ser Lys Gly Arg Ala Arg Arg Ala Gly Ser Arg Tyr			
485		490	495
Val Ile Thr Val Glu Glu Lys			
500			

<210> 16
 <211> 549
 <212> PRT
 <213> arabidopsis thaliana

<400> 16			
Glu Lys Val Val Glu Glu Gln Ala Arg Arg Tyr Gln Leu Asp Val Leu			
1	5	10	15
Glu Gln Ala Lys Ala Lys Asn Thr Ile Ala Phe Leu Glu Thr Gly Ala			
20	25	30	
Gly Lys Thr Leu Ile Ala Ile Leu Leu Ile Lys Ser Val His Lys Asp			
35	40	45	
Leu Met Ser Gln Asn Arg Lys Met Leu Ser Val Phe Leu Val Pro Lys			
50	55	60	
Val Pro Leu Val Tyr Gln Gln Ala Glu Val Ile Arg Asn Gln Thr Cys			
65	70	75	80
Phe Gln Val Gly His Tyr Cys Gly Glu Met Gly Gln Asp Phe Trp Asp			
85	90	95	
Ser Arg Arg Trp Gln Arg Glu Phe Glu Ser Lys Gln Val Leu Val Met			
100	105	110	
Thr Ala Gln Ile Leu Leu Asn Ile Leu Arg His Ser Ile Ile Arg Met			
115	120	125	
Glu Thr Ile Asp Leu Leu Ile Leu Asp Glu Cys His His Ala Val Lys			
130	135	140	
Lys His Pro Tyr Ser Leu Val Met Ser Glu Phe Tyr His Thr Thr Pro			
145	150	155	160
Lys Asp Lys Arg Pro Ala Ile Phe Gly Met Thr Ala Ser Pro Val Asn			
165	170	175	
Leu Lys Gly Val Ser Ser Gln Val Asp Cys Ala Ile Lys Ile Arg Asn			
180	185	190	
Leu Glu Thr Lys Leu Asp Ser Thr Val Cys Thr Ile Lys Asp Arg Lys			
195	200	205	
Glu Leu Glu Lys His Val Pro Met Pro Ser Glu Ile Val Val Glu Tyr			
210	215	220	
Asp Lys Ala Ala Thr Met Trp Ser Leu His Glu Thr Ile Lys Gln Met			
225	230	235	240
Ile Ala Ala Val Glu Glu Ala Ala Gln Ala Ser Ser Arg Lys Ser Lys			
245	250	255	
Trp Gln Phe Met Gly Ala Arg Asp Ala Gly Ala Lys Asp Glu Leu Arg			
260	265	270	

Gln Val Tyr Gly Val Ser Glu Arg Thr Glu Ser Asp Gly Ala Ala Asn
 275 280 285
 Leu Ile His Lys Leu Arg Ala Ile Asn Tyr Thr Leu Ala Glu Leu Gly
 290 295 300
 Gln Trp Cys Ala Tyr Lys Val Gly Gln Ser Phe Leu Ser Ala Leu Gln
 305 310 315 320
 Ser Asp Glu Arg Val Asn Phe Gln Val Asp Val Lys Phe Gln Glu Ser
 325 330 335
 Tyr Leu Ser Glu Val Val Ser Leu Leu Gln Cys Glu Leu Leu Glu Gly
 340 345 350
 Ala Ala Ala Glu Lys Val Ala Ala Glu Val Gly Lys Pro Glu Asn Gly
 355 360 365
 Asn Ala His Asp Glu Met Glu Glu Gly Glu Leu Pro Asp Asp Pro Val
 370 375 380
 Val Ser Gly Gly Glu His Val Asp Glu Val Ile Gly Ala Ala Val Ala
 385 390 395 400
 Asp Gly Lys Val Thr Pro Lys Val Gln Ser Leu Ile Lys Leu Leu
 405 410 415
 Lys Tyr Gln His Thr Ala Asp Phe Arg Ala Ile Val Phe Val Glu Arg
 420 425 430
 Val Val Ala Ala Leu Val Leu Pro Lys Val Phe Ala Glu Leu Pro Ser
 435 440 445
 Leu Ser Phe Ile Arg Cys Ala Ser Met Ile Gly His Asn Asn Ser Gln
 450 455 460
 Glu Met Lys Ser Ser Gln Met Gln Asp Thr Ile Ser Lys Phe Arg Asp
 465 470 475 480
 Gly His Val Thr Leu Leu Val Ala Thr Ser Val Ala Glu Glu Gly Leu
 485 490 495
 Asp Ile Arg Gln Cys Asn Val Val Met Arg Phe Asp Leu Ala Lys Thr
 500 505 510
 Val Leu Ala Tyr Ile Gln Ser Arg Gly Arg Ala Arg Lys Pro Gly Ser
 515 520 525
 Asp Tyr Ile Leu Met Val Glu Arg Gly Asn Val Ser His Ala Ala Phe
 530 535 540
 Leu Arg Asn Ala Arg
 545

<210> 17
 <211> 485
 <212> PRT
 <213> schizosaccharomyces pombe

<400> 17
 Ser Phe Leu Leu Pro Gln Leu Leu Arg Lys Tyr Gln Gln Asp Val Tyr
 1 5 10 15
 Asn Ile Ala Ser Lys Gln Asn Thr Leu Leu Val Met Arg Thr Gly Ala
 20 25 30
 Gly Lys Thr Leu Leu Ala Val Lys Leu Ile Lys Gln Lys Leu Glu Glu
 35 40 45
 Gln Ile Leu Ile Gln Glu Ser Asn Leu Glu His Lys Lys Ile Ser Val
 50 55 60
 Phe Leu Val Asn Lys Val Pro Leu Val Phe Gln Gln Ala Glu Tyr Ile
 65 70 75 80
 Arg Ser Gln Leu Pro Ala Lys Val Gly Met Phe Tyr Gly Glu Leu Ser
 85 90 95
 Ile Glu Met Ser Glu Gln Leu Leu Thr Asn Ile Ile Leu Lys Tyr Asn

100 105 110
Val Ile Val Ile Thr Ala Asp Leu Phe Tyr Leu Phe Leu Ala Arg Gly
115 120 125
Phe Leu Ser Ile Asn Asp Leu Asn Leu Ile Ile Phe Asp Glu Cys His
130 135 140
His Ala Ile Gly Asn Asp Ala Tyr Ala Arg Ile Met Asn Asp Phe Tyr
145 150 155 160
His Arg Ala Lys Ala Val Leu Ser Lys Lys His Phe Thr Leu Pro Arg
165 170 175
Ile Phe Gly Met Thr Ala Ser Pro Phe Thr Gly Lys Lys Gly Asn Leu
180 185 190
Tyr His Arg Leu Tyr Gln Trp Glu Gln Leu Phe Asp Ser Lys Ala His
195 200 205
Val Val Ser Glu Asn Glu Leu Ala Asp Tyr Phe Cys Leu Pro Glu Glu
210 215 220
Ser Tyr Val Met Tyr Ser Asn Lys Leu Val Val Pro Pro Ser Asp Ser
225 230 235 240
Ile Ile Lys Lys Cys Glu Glu Thr Leu Gln Gly Cys Lys Leu Ile Ser
245 250 255
Arg Ala Val Lys Thr Ala Leu Ala Glu Thr Ile Asp Met Gly Leu Trp
260 265 270
Phe Gly Glu Gln Val Trp Leu Tyr Leu Val Asp Phe Val Glu Thr Lys
275 280 285
Arg Leu Lys Lys Lys Ala Leu Gly Lys Gln Leu Ser Asp Asp Glu Glu
290 295 300
Leu Ala Ile Asp Arg Leu Lys Ile Phe Val Glu Asp Trp Lys Asn Asn
305 310 315 320
Lys Tyr Ser Asp Asn Gly Pro Arg Ile Pro Val Phe Asp Ser Thr Asp
325 330 335
Val Thr Asp Lys Val Phe Lys Leu Leu Glu Leu Leu Lys Ala Thr Tyr
340 345 350
Arg Lys Ser Asp Ser Val Arg Thr Val Ile Phe Val Glu Arg Lys Ala
355 360 365
Thr Ala Phe Thr Leu Ser Leu Phe Met Lys Thr Leu Asn Leu Pro Asn
370 375 380
Ile Arg Ala His Ser Phe Ile Gly His Gly Pro Ser Asp Gln Gly Glu
385 390 395 400
Phe Ser Met Thr Phe Arg Arg Gln Lys Asp Thr Leu His Lys Phe Lys
405 410 415
Thr Gly Lys Tyr Asn Val Leu Ile Ala Thr Ala Val Ala Glu Glu Gly
420 425 430
Ile Asp Val Pro Ser Cys Asn Leu Val Ile Arg Phe Asn Ile Cys Arg
435 440 445
Thr Val Thr Gln Tyr Val Gln Ser Arg Gly Arg Ala Arg Ala Met Ala
450 455 460
Ser Lys Phe Leu Ile Phe Leu Asn Thr Glu Glu Leu Leu Ile His Glu
465 470 475 480
Arg Ile Leu His Glu
485

Genes